

1	CCAGATTCCCATAAAGCACATGGTCTAATCTGTTACGTAACAGCAAGACA	50
51	GCGTCACCTCACCTGTTCTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAG	109
110	ACCACCAGGCTGAGTATCCTGACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGG	168
169	GAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTGCG .ATG AAA	225
1	Met Lys	2
226	GTT CTA ATC TCT TCC CTC CTC CTG TTG CTG CCA CTA ATG CTG ATG	270
3	Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu Met	17
271	TCC ATG GTC TCT AGC AGC CTG AAT CCA GGG GTC GCC AGA GGC CAC	315
18	Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His	32
316	AGG GAC CGA GGC CAG GCT TCT AGG AGA TGG CTC CAG GAA GGC GGC	360
33	Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly	47
361	CAA GAA TGT GAG TGC AAA GAT TGG TTC CTG AGA GCC CCG AGA AGA	405
48	Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg	62
406	AAA TTC ATG ACA GTG TCT GGG CTG CCA AAG AAG CAG TGC CCC TGT	450
63	Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys Pro Cys	77
451	GAT CAT TTC AAG GGC AAT GTG AAG AAA ACA AGA CAC CAA AGG CAC	495
78	Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln Arg His	92
496	CAC AGA AAG CCA AAC AAG CAT TCC AGA GCC TGC CAG CAA TTT CTC	540
93	His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Gln Phe Leu	107
541	AAA CAA TGT CAG CTA AGA AGC TTT GCT CTG CCT TTG TAG GAGCTCT	586
108	Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu ***	119
587	GAGCGCCCACTCTTCCAATTAACATTCTCAAAAAGCATGTTTTTCAAGATCATTTTGT	645
646	TTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTAC	704
705	CCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGT	763
764	CATTTAACCTTAAATGAATCAGGAAAGTAGCAAAACAGAAGTCAATAAATATTTTTAA	822
823	TGTCACAGAAAAAAAAAAAAAAAAAAAA	849

Fig. 2

1 ATTAATTGTGCCACACTACGCCACCTGAGCAGTGACAGGAAATCAGAAGCCTCTCGCT 60
 61 GGTGACAGTCCCCACAGTCCTTAAGAAACAGCAGACAGCCGCA ATG AAG CTT CTA 116
 1 Met Lys Leu Leu 4

 117 GCC TCT CCC TTC CTT CTG TTG CTG ACA GGG ATG TTC ACG GCC ACG 161
 5 Ala Ser Pro Phe Leu Leu Leu Leu Thr Gly Met Phe Thr Ala Thr 19

 162 GTC TCC AGC AGC CCG AAT CAA GAG GTC GCC AGA CAC CAT GGG GAT 206
 20 Val Ser Ser Ser Pro Asn Gln Glu Val Ala Arg His His Gly Asp 34

 207 CAA CAC CAG GCT CCT AGG AGG TGG CTC TGG GAA GGT GGC CAA GAG 251
 35 Gln His Gln Ala Pro Arg Arg Trp Leu Trp Glu Gly Gly Gln Glu 49

 252 TGT GAC TGC AAA GAT TGG TCC CTG CGA GTC TCA AAG AGA AAA ACC 296
 50 Cys Asp Cys Lys Asp Trp Ser Leu Arg Val Ser Lys Arg Lys Thr 64

 297 ACA GCA GTG CTG GAG CCA CCA AGG AAG CAG TGT CCC TGT GAT CAT 341
 65 Thr Ala Val Leu Glu Pro Pro Arg Lys Gln Cys Pro Cys Asp His 79

 342 GTC AAG GGC AGT GAG AAA AAG AAC AGA CGC CAA AAG CAC CAC AGG 386
 80 Val Lys Gly Ser Glu Lys Lys Asn Arg Arg Gln Lys His His Arg 94

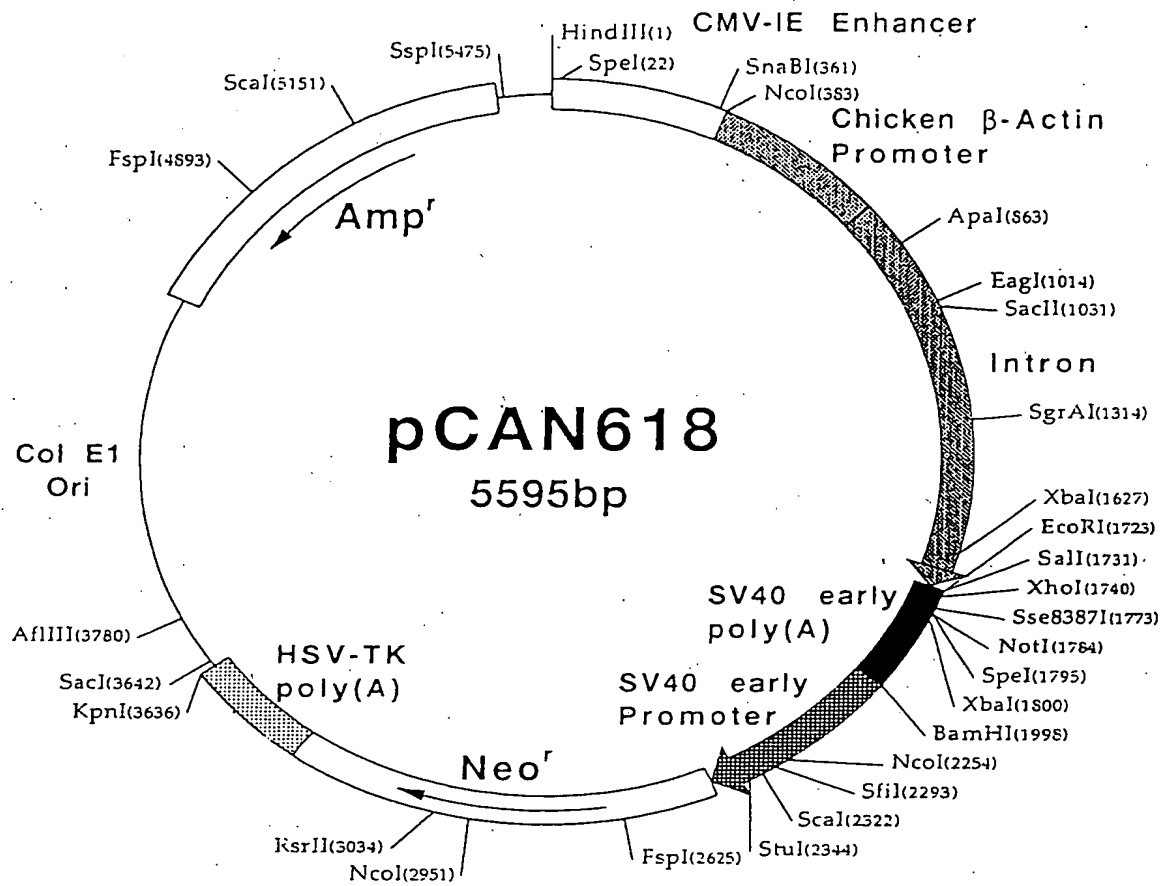
 387 AAG TCA CAA AGG CCC TCC AGA ACC TGC CAG CAA TTT CTC AAG CGA 431
 95 Lys Ser Gln Arg Pro Ser Arg Thr Cys Gln Gln Phe Leu Lys Arg 109

 432 TGT CAA CTA GCA AGC TTC GGC CTG CCC TTA TAG TTCCGAGACTCTGCC 479
 110 Cys Gln Leu Ala Ser Phe Ala Leu Pro Leu *** 119

 480 CTCCAGCTAGGCTCTCTCAATGAGAGGGAGATGATCATCCTTGGAGCGCTTCTTATCCCC 539
 540 CCACCCCATCCTCACCAAGAGCACCCAGCGCTCTCGAAGGCACGGCCAGCTGTGTAC 599
 600 CTGCCACTGTGTCCTCTGCACTTGTCACTCTTCTTACATGCCTTCTGTCCGGGGTCTAAA 659
 660 AGGCAGGTGAAGCACTGAATCAGAGACTGCCTGGTTAGAAGCAATAAAGGTTTAGAAATT 719
 720 GTGGTTTCTTAGCATCTAGACAACCTTCAGTGTTTATGGTTCTGTGCATCATCATCATCA 779
 780 TCACCACCACCCTCATCACTACCCCATCATTATCACTGCACTCTGTGGGTCTCTAACAC 839
 840 AGTACAAGAGATATAAATGCAGAAGCACAGCTCGAGGCTAGAAAGATGGAAGGAGGATC 899
 900 CCAGCTGCCATTCAAAAGGGTTTTGAACCAATAAAACAGAATGGCATCCGCAAAAAAAA 959

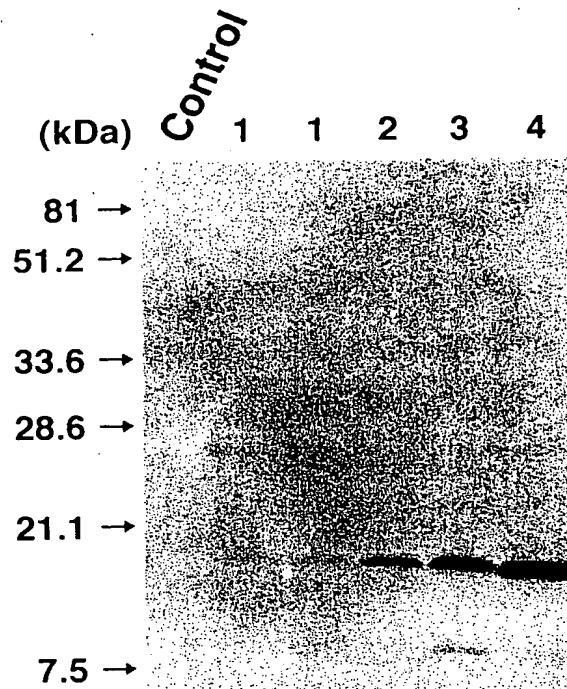
1	AGCAGTTACAAGAAATCAGAAGCCTCTAACTGGTGACAATCCACACAGCCTTTAAGAACC	60
61	AACAGACAGCC ACA ATG AAG CTT CTA GCC TCT CCC TTC CTT CTG TTG	107
1	Met Lys Leu Leu Ala Ser Pro Phe Leu Leu Leu	11
	↓	
108	CTT CCA GTG ATG CTC ATG TCC ATG GTC TTC AGC AGC CCG AAC CCA	152
12	Leu Pro Val Met Leu Met Ser Met Val Phe Ser Ser Pro Asn Pro	26
153	GGG GTC GCC AGA AGC CAC GGG GAC CAA CAC CTG GCT CCT AGG AGG	197
27	Gly Val Ala Arg Ser His Gly Asp Gln His Leu Ala Pro Arg Arg	41
198	TGG CTC TTG GAA GGT GGC CAA GAA TGT GAA TGC AAA GAT TGG TTC	242
42	Trp Leu Leu Glu Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe	56
243	CTG CAA GCC CCA AAG AGA AAA GCC ACA GCA GTG CTG GGG CCA CCA	287
57	Leu Gln Ala Pro Lys Arg Lys Ala Thr Ala Val Leu Gly Pro Pro	71
288	AGG AAG CAG TGT CCC TGT GAT CAC GTC AAG GGC AGG GAG AAA AAA	332
72	Arg Lys Gln Cys Pro Cys Asp His Val Lys Gly Arg Glu Lys Lys	86
333	AAC AGA CAC CAA AAG CAC CAC AGG AAG TCG CAA AGA CCC TCC AGA	377
87	Asn Arg His Gln Lys His His Arg Lys Ser Gln Arg Pro Ser Arg	101
378	GCC TGC CAG CAA TTT CTC AAA CGA TGT CAC CTG GCA AGC TTT GCG	422
102	Ala Cys Gln Gln Phe Leu Lys Arg Cys His Leu Ala Ser Phe Ala	116
423	CTG CCC TTA TAG TACTGAGACTCTGCTCCTCTAGTTAGACTCTCTCAGTGGAAGG	478
117	Leu Pro Leu ***	119
479	AGGTGACCAGCCCTAGCACGGTTCTTATTCTCCCCACCCCCATCCTCACCAAGAGCACCC	538
539	CAGTGCTCTCTGAAGGCACTGCCTCACAGTGTATCTATGACTGTGCCCTAGTGCCGGCT	598
599	GCACTTGCCACTCTTGTCTTATGCCTTCTGTTTACCCTACAAGAATGCAGGACACCTCGG	658
659	CCTCCTGTTGGCCTCACATTGCAATCAGAAAACTTGCAATGAAAATAATTAATACATAG	718
719	TGCATACGTGTGTGTAAAAA	764

Fig. 4



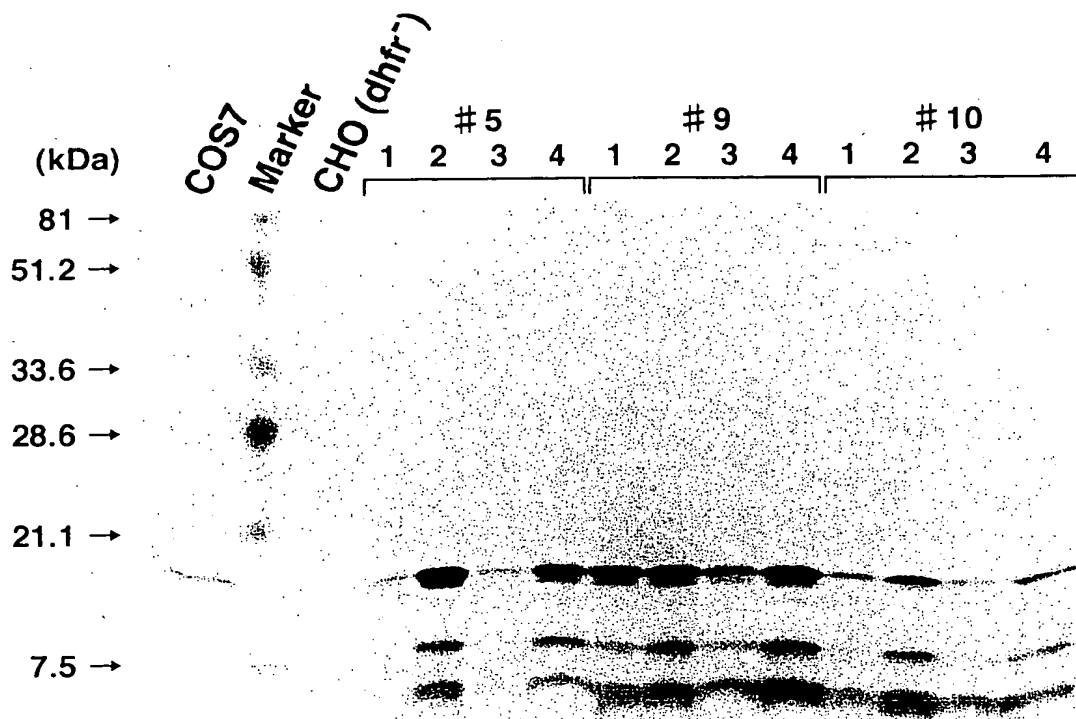
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Fig. 5



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Fig. 6



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Fig. 7

